

RESULT	2		
Q9SEW4			
ID	Q9SEW4	PRELIMINARY:	PRT: 593 AA.
AC	Q9SEW4		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, last annotation update)		
DE	VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).		
OS	Juglans regia (English walnut).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;		
OC	Fagales; Juglandaceae; Juglans.		
OX	NCBI_TaxID=51240;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. SONLAD; TISSUE=SONATIC EMBRYO LINE;		
RA	Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;		
RT	"Identification and cloning of a cDNA encoding a vicilin-like protein,		
RT	Jug r 2, from English walnut kernel (Juglans regia): a major food		
RT	allergen."		
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF066055; AAF18269.1; -		
DR	HSSP; P02853; 2PHL.		
DR	INTERPRO; IPR001113; -		
DR	PFAM; PF00546; Seedstore_7s; 1.		
FT	NON_TER		
SO	SEQUENCE	593 AA: 69990 MW: 99A127E19B18C0D8 CRC64:	

Query Match	52.28;	Score 117.5;	DB 10;	Length 593;
Best Local Similarity	46.38;	Pred. No. 8.6e-07;		
Matches 19;	Conservative 14;	Mismatches 7;	Indels 1;	Gaps 1;

OY 1 PEDPQRRIECCQEEC-RQEEERDOPQCOCRLKRFEEQOO 40
| | | : | | | : | : : | | : | : | : :
Db 69 PRDPFRGVECCQQCEGRRGQEQTLCRRCRCEGRRQEEENE 109

RESULT	3	
Q9SP15		
ID	Q9SP15	PRELIMINARY; PRT; 666 AA.
AC	Q9SP15;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DF	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)	
DE	VICILIN PRECURSOR.	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
OX	NCBI_TaxID=60698;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=NUT KERNEL;	
RA	Marcus J.P., Goulier K.C., Green J.L., Manners J.M.;	
RT	"A family of antimicrobial peptides is produced by processing of a 7S	
RT	globulin protein in Macadamia integrifolia kernels."	
RL	Plant J. 0:0-0(1999).	
DR	EMBL; AF161883; AAD54244.1; -.	
DR	HSSP; P02853; 2PHT.	
DR	INTERPRO; IPR001113; -.	
DR	PFAM; PF00546; SeedsTree_7s.1.	
SO	SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64;	

Query Match	50.7%	Score 114	DB 10	Length 666
Best Local Similarity	47.5%	Pred. No. 2.5e-06		
Matches 19	Conservative 11	Mismatches 8	Indels 2	Gaps 1
QY	3	DPORYECCQOEC--RODEERQOPCCQRCRLKRFDEQDQ	40	
	: : :			
		: :	: : :	:

Db 121 DPOQYEOCKHCQRETEPRHMQTCQRCERRYEKEKR 160

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RESULT 4
Q9SPJ3 PRELIMINARY; PRT; 625 AA.
ID Q9SPJ3
AC Q9SPJ3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).
GN Amp2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=NUIT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7
RL globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999).
DR EMBL; AF161885; AAD54246.1; -.
DR HSSP; P02853; 2PHL.
DR INTERPRO; IPR001113; -.
DR PFM; PF00546; Seedstore_7s; 1.
FT NON_TER 1
SEQUENCE 625 AA: 73586 MW; 415808A89D370296 CRC64;

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Query Match	49.8%;	Score 112;	DB 10;	Length 625;
Best Local Similarity	47.5%;	Pred. No. 4.2e-06;		
Matches 19;	Conservative 11;	Mismatches 8;	Indels 2;	Gaps 1;

Dy 3 DQQRRYECCQQEC--RQEEKQGPGCCGRCLKEEQEQDQ 40
| | | | : | | | | | | | | : | | : |
Db 80 DPQQYEGCCKRGQRRETFPRMHIQCQRCERTEKEKK 110

ID	Q9SPLA	PRELIMINARY:	PRT:	666 AA.
AC	Q9SPLA;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	VITILIN PRECURSOR.			
GN	AMP2.			
OS	Macadamia integrifolia (Macadamia nut).			
OC	Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;			
CC	Magnoliophyta: eudicotyledons: Proteaceae; Macadamia.			
OX	NCBI_TaxID=60698;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=NUIT KERNEL;			
RA	Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;			
RT	"A family of antimicrobial peptides is produced by processing of a 7S			
RL	globulin protein in Macadamia integrifolia.";			
PL	Plant J. 0:0-0(1999).			
DR	HMBL; AF161884; AAD54245.1; -;			
DR	HSSP; P02853; ZPHL.			
DR	INTERPRO: IPR001113; -;			
DR	PFAM: PF00546; Seedstore_7s; 1.			
SO	SEQUENCE 666 AA; 78243 MW; OECA22F8710F8A7B CRC64;			

Query Match	49.8%	Score 112	DB 10	Length 666	
Best Local Similarity	56.4%	Pred. No. 4.4e-06			
Matches 22	Conservative 7	Mismatches 4	Indels 6	Gaps 2	
0Y	3	DPRR-VFECQECRQCEERQPPCCQGCCLKRFEEQQQ	40		

DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DE TATA BOX-BINDING PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=92350691; PubMed=1641350;
RA Hashimoto S., Fujita H., Hasegawa S., Roeder R.G., Horikoshi M.,
RT "Conserved structural motifs within the N-terminal domain of TFIID tau
from Xenopus, mouse and human."
RL Nucleic Acids Res. 20:3788-3788(1992).
SQ SEQUENCE 154 AA; 16790 MW; 93A5A0B5C6AFC604 CRC64;

Query Match 36.4%; Score 82; DB 4; Length 154;
Best Local Similarity 41.0%; Pred. No. 0.0057;
Matches 16; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

OY 2 EDPORRYECCOECROEERQOPQCOORCLKRFEEQOQ 40
|: ||:: ||: ||::|| ||: ||: ||: ||:
Db 53 EEOQRQOQOQOQOQOQOQOQOQOQOQOQOQOQ 91

RESULT 10

ID 016845 PRELIMINARY; PRT; 339 AA.
AC Q16845;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-JUN-1998 (TReMBLrel. 06, last sequence update)
DE 01-MAY-2000 (TReMBLrel. 13, last annotation update)
DE TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA
DE SEQUENCE-BINDING PROTEIN) (TBP).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROBLAST;
RA Kao C., Lieberman P., Schmidt M., Zhou Q., Pei R., Berk A.J.;
RA Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
CC OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIID BINDS
CC SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO
CC THE POSITION OF TRANSCRIPTION INITIATION.
CC -1- SUBUNIT: BINDS DNA AS A MONOMER.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: THE C-TERMINAL 180 RESIDUES ARE EXTREMELY WELL
CC CONSERVED IN ALL EUKARYOTIC TFIID
CC -1- SIMILARITY: WEAK, WITH BACTERIAL POLYMERASE SIGMA-FACTORS.
DR EMBL: M4960; AAC03409.1; -.
DR HSSP: P20226; ITGH.
DR INTERPRO: IPR000814; -.
DR PFAM: PF00352; TBP; 2.
DR PRINTS: PR00686; TIFACTORIID.
DR PROSITE: PS00351; TFIID; 2.
KW Transcription regulation; DNA-binding; Nuclear protein; Duplication.
SQ SEQUENCE 339 AA; 37783 MW; 98B7E26CB42B853A CRC64;

Query Match 36.4%; Score 82; DB 4; Length 339;
Best Local Similarity 41.0%; Pred. No. 0.011;
Matches 16; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

OY 2 EDPORRYECCOECROEERQOPQCOORCLKRFEEQOQ 40
|: ||:: ||: ||::|| ||: ||: ||: ||:
Db 53 EEOQRQOQOQOQOQOQOQOQOQOQOQOQOQOQ 91

RESULT 11

ID 090957 PRELIMINARY; PRT; 2123 AA.
AC Q90957;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, last annotation update)
DE ADENYLYL CYCLASE.
GN ACRA.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Dictyostellida; Dictyostellium.
ON NCBI_TaxID=44689;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Soderbom F., Anjard C., Tranfar N., Loomis W.F.;
RT "An adenylyl cyclase that functions during late development of
RT Dictyostellium."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF153362; AAD50121.1; -.
DR HSSP: P19754; JAWK.
DR INTERPRO: IPR000410; -.
DR INTERPRO: IPR001054; -.
DR INTERPRO: IPR001440; -.
DR INTERPRO: IPR001596; -.
DR INTERPRO: IPR001789; -.
DR PFAM: PF00072; response_reg; 1.
DR PFAM: PF00211; guanylate_cyc; 1.
DR PRINTS: PR00344; BCTRENSOR.
DR PROSITE: PS00387; PPAASE; UNKNOWN_1.
SQ SEQUENCE 2123 AA; 243039 MW; 744247140BC342FA CRC64;

Query Match 36.2%; Score 81.5; DB 5; Length 2123;
Best Local Similarity 43.6%; Pred. No. 0.056;
Matches 17; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

OY 2 EDPORRYECCOECROEERQOPQCOORCLKRFEEQOQ 40
|: ||:: ||: ||::|| ||: ||: ||: ||:
Db 1932 QOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 1969

RESULT 12

ID Q9W352 PRELIMINARY; PRT; 663 AA.
AC Q9W352;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, last annotation update)
DE CG17446 PROTEIN.
GN CG17446.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Planckoch C., Baldwin D.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doop L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwu C.,
RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Schebler F., Shen H.,
RA Shue B.C., Sideri-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Vector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL: AEO03446; AAF64683.1; -
DR FLYBASE: FBgn0030121; CG17446.
DR INTERPRO: IPR001965; -
DR PFM; PF00628; PBD; 1.
SQ SEQUENCE 663 AA; 76696 MW; 8573CD209AE28157 CRC64;

	Query Match Similarity	36.0%	Score 81:	DB 5:	Length 669:
	Best Local Similarity	41.0%	Pred. No. 0.025:		
	Matches 16:	Conservative 13:	Mismatches 10:	Indels 0:	Gaps 0:
QY	2 EDPORRYECOECHRCQERODPQCOCRLKRFEGEDQQQ 40				
	: 1:: :: 11: :11:: 1111 11: :: :111111				
Dh	587 0000000000000000000001DQP0000000000QE000 625				
RESULT	13				
O9W3A1					
ID	O9W3A1	PRELIMINARY;	PRT,	821 AA.	
AC	O9W3A1;				
DT	01-MAY-2000 (TRENBLREL. 13; Created)				
DT	01-MAY-2000 (TRENBLREL. 13; Last sequence update)				
DT	01-MAY-2000 (TRENBLREL. 13; Last annotation update)				
DE	CG15365 PROTEIN.				
CN	CG15365.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
CC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCHI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	STRAIN-BERKELEY;				
RX	MEDLINE=20196006; PubMed=10731132;				
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherier S.E., Li P.W., Hoskins R.A., Galie R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos D.G.,				
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,				
RA	Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				

RA Beeson K.Y., Benos P.V., Berman H.P., Bhandari P., Bolshakov S.,
RA Bokorova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chanora I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pallos B., Deitcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dublin K.J., Evangelista C.C., Ferriz C., Ferreira S., Fleischmann W.,
RA Flocker C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Foster A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman I.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matteli B., McIntosh T.C., McLeod M.P., Mopherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacied J.M.,
RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Slden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Wotley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*." ,
RL Science 287:2185-2195(2000).
DR FLYBASE, AE003446; AAF6433.1; -
DR EMBL; FB00030077; CG15365.
SQ SEQUENCE 821 AA: 91909 MW: EAAVBE72FEC5CB88 CRC64;

[illegible]

